

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANTS: Katia Georgopoulos
Bruce Morgan

10

(ii) TITLE OF INVENTION: The Aiolos Gene

(iii) NUMBER OF SEQUENCES: 22

(iv) CORRESPONDENCE ADDRESS:

15

(A) ADDRESSEE: LAHIVE & COCKFIELD
(B) STREET: 60 State Street, Suite 510
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02109-1875

20

(v) COMPUTER READABLE FORM:

25

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

35

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Myers, Louis
(B) REGISTRATION NUMBER: 35,965
(C) REFERENCE/DOCKET NUMBER: MGP-042-2

40

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 227-7400
(B) TELEFAX: (617) 227-5941

(2) INFORMATION FOR SEQ ID NO:1:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1984 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 374..1895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

0650220" 020599

CACGAGCGCA CACCGCTCGG CTCTCCTTGC GACACGCCCT CATCCCCGGT GTTTCTCAAG
60

5 TAGACGTCCC GAGACGGTCG CTGAGGCACT GTTTCCACGC GATCAGGGTT CCTCAGGCTT
120

GACATTCAAA AGTGGGTGCG GAACCCGCGG CACTCGGAGC GTGCTTTAAA GCGGCCGCCA
180

10 GCCAGCGCCG CTCTAACCTC GCGCCCCGGC TGCCGGCGGC TCCCGCCCTG CATCTGCGCC
240

15 GACGCGACCG AGCGATCCCG GGGCCTCCCT GCGCCCGGAA TCTCCCGCCA GCCGCGCGGG
300

TCCCCACGGC AGCAGCACGT GGAGCGGCCG CGGAGCCTGA GCGACAGCTG CAGCCCGCGC
360

20 GGCCCGCGGC GAC ATG GAA GAT ATA CAA CCG ACT GTG GAG CTG AAA AGC
409

Met Glu Asp Ile Gln Pro Thr Val Glu Leu Lys Ser
1 5 10

25 ACG GAG GAG CAG CCT CTG CCC ACA GAG AGC CCA GAC GCT CTG AAT GAC
457

Thr Glu Glu Gln Pro Leu Pro Thr Glu Ser Pro Asp Ala Leu Asn Asp
15 20 25

30 TAC AGC TTG CCC AAA CCT CAT GAG ATA GAA AAC GTG GAC AGT AGA GAA
505

Tyr Ser Leu Pro Lys Pro His Glu Ile Glu Asn Val Asp Ser Arg Glu
30 35 40

35 GCC CCA GCC AAT GAA GAC GAA GAT GCA GGA GAA GAT TCG ATG AAA GTG
553

Ala Pro Ala Asn Glu Asp Glu Asp Ala Gly Glu Asp Ser Met Lys Val
45 50 55 60

40 AAA GAT GAA TAC AGC GAC AGA GAT GAG AAC ATT ATG AAG CCG GAG CCC
601

Lys Asp Glu Tyr Ser Asp Arg Asp Glu Asn Ile Met Lys Pro Glu Pro
65 70 75

45 ATG GGA GAT GCA GAA GAG AGT GAA ATG CCT TAC AGC TAT GCA AGA GAA
649

Met Gly Asp Ala Glu Glu Ser Glu Met Pro Tyr Ser Tyr Ala Arg Glu
80 85 90

50 TAC AGC GAC TAT GAA AGC ATT AAG CTG GAG AGA CAC GTG CCC TAT GAC
697

Tyr Ser Asp Tyr Glu Ser Ile Lys Leu Glu Arg His Val Pro Tyr Asp
95 100 105

55 AAC AGC AGA CCA ACC AGT GGG AAG ATG AAC TGC GAC GTG TGC GGG TTA
745

Asn Ser Arg Pro Thr Ser Gly Lys Met Asn Cys Asp Val Cys Gly Leu

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	110	115	120
	TCC TGC ATT AGC TTC AAC GTC TTG ATG GTT CAT AAG CGA AGC CAT ACC		
	793		
5	Ser Cys Ile Ser Phe Asn Val Leu Met Val His Lys Arg Ser His Thr		
	125	130	135 140
	GGC GAA CGC CCG TTC CAG TGT AAT CAG TGC GGG GCA TCT TTT ACT CAG		
	841		
10	Gly Glu Arg Pro Phe Gln Cys Asn Gln Cys Gly Ala Ser Phe Thr Gln		
		145	150 155
	AAA GGT AAC CTC CTC CGT CAT ATT AAA CTG CAC ACG GGG GAA AAA CCT		
	889		
15	Lys Gly Asn Leu Leu Arg His Ile Lys Leu His Thr Gly Glu Lys Pro		
		160	165 170
	TTT AAG TGT CAC CTC TGC AAC TAC GCA TGC CAA AGG AGA GAT GCG CTC		
	937		
20	Phe Lys Cys His Leu Cys Asn Tyr Ala Cys Gln Arg Arg Asp Ala Leu		
		175	180 185
	ACG GGA CAC CTT AGG ACA CAT TCT GTG GAG AAG CCG TAC AAG TGT GAG		
	985		
25	Thr Gly His Leu Arg Thr His Ser Val Glu Lys Pro Tyr Lys Cys Glu		
		190	195 200
	TTC TGC GGA AGA AGC TAC AAG CAG AGA AGC TCC CTG GAG GAG CAC AAG		
	1033		
30	Phe Cys Gly Arg Ser Tyr Lys Gln Arg Ser Ser Leu Glu Glu His Lys		
	205	210	215 220
	GAA CGC TGC CGA GCT TTT CTT CAG AAC CCT GAC CTG GGG GAC GCT GCA		
	1081		
35	Glu Arg Cys Arg Ala Phe Leu Gln Asn Pro Asp Leu Gly Asp Ala Ala		
		225	230 235
	AGT GTG GAG GCA AGA CAC ATC AAA GCC GAG ATG GGA AGT GAG AGA GCT		
	1129		
40	Ser Val Glu Ala Arg His Ile Lys Ala Glu Met Gly Ser Glu Arg Ala		
		240	245 250
	CTC GTC CTG GAC AGA TTA GCA AGC AAT GTG GCT AAG CGA AAA AGC TCG		
	1177		
45	Leu Val Leu Asp Arg Leu Ala Ser Asn Val Ala Lys Arg Lys Ser Ser		
		255	260 265
	ATG CCT CAG AAA TTC ATC GGT GAG AAG CGG CAC TGC TTC GAT GCC AAC		
	1225		
50	Met Pro Gln Lys Phe Ile Gly Glu Lys Arg His Cys Phe Asp Ala Asn		
		270	275 280
	TAC AAT CCC GGC TAC ATG TAC GAG AAG GAG AAC GAG ATG ATG CAG ACC		
	1273		
55	Tyr Asn Pro Gly Tyr Met Tyr Glu Lys Glu Asn Glu Met Met Gln Thr		
	285	290	295 300

09019348 020598

CGG ATG ATG GAC CAA GCC ATC AAT AAC GCC ATC AGC TAT CTA GGG GCT
1321
Arg Met Met Asp Gln Ala Ile Asn Asn Ala Ile Ser Tyr Leu Gly Ala
305 310 315

5 GAA GCC TTC CGC CCC TTA GTC CAG ACT CCG CCT GCT CCC ACC TCT GAG
1369
Glu Ala Phe Arg Pro Leu Val Gln Thr Pro Pro Ala Pro Thr Ser Glu
320 325 330

10 ATG GTC CCA GTC ATC AGC AGT GTG TAC CCC ATA GCA CTT ACT CGG GCC
1417
Met Val Pro Val Ile Ser Ser Val Tyr Pro Ile Ala Leu Thr Arg Ala
335 340 345

15 GAT ATG CCA ATG GGG GCC CCG CAG GAG ATG GAA AAG AAA CGG ATC CTC
1465
Asp Met Pro Met Gly Ala Pro Gln Glu Met Glu Lys Lys Arg Ile Leu
350 355 360

20 CTG CCA GAG AAG ATC TTG CCT TCT GAA CGA GGT CTG TCC CCC AAT AAC
1513
Leu Pro Glu Lys Ile Leu Pro Ser Glu Arg Gly Leu Ser Pro Asn Asn
365 370 375 380

25 AGT GCC CAG GAC TCC ACA GAC ACC GAC AGC AAC CAC GAG GAT CGC CAA
1561
Ser Ala Gln Asp Ser Thr Asp Thr Asp Ser Asn His Glu Asp Arg Gln
385 390 395

30 CAT CTC TAC CAG CAA AGC CAC GTG GTC CTC CCC CAG GCC CGC AAT GGG
1609
His Leu Tyr Gln Gln Ser His Val Val Leu Pro Gln Ala Arg Asn Gly
400 405 410

35 ATG CCT CTT CTG AAG GAG GTC CCT CGC TCT TTT GAA CTC CTC AAG CCC
1657
Met Pro Leu Leu Lys Glu Val Pro Arg Ser Phe Glu Leu Leu Lys Pro
415 420 425

40 CCT CCC ATC TGC CTG AGG GAC TCC ATC AAA GTG ATC AAC AAA GAA GGG
1705
Pro Pro Ile Cys Leu Arg Asp Ser Ile Lys Val Ile Asn Lys Glu Gly
430 435 440

45 GAG GTG ATG GAT GTG TTT CGA TGT GAC CAC TGC CAC GTC CTC TTC CTA
1753
Glu Val Met Asp Val Phe Arg Cys Asp His Cys His Val Leu Phe Leu
445 450 455 460

50 GAT TAT GTG ATG TTC ACC ATC CAC ATG GGG TGC CAT GGT TTC CGT GAT
1801
Asp Tyr Val Met Phe Thr Ile His Met Gly Cys His Gly Phe Arg Asp
465 470 475

55 CCC TTT GAG TGT AAC ATG TGT GGC TAT CGA AGC CAC GAT CGC TAT GAG
1849

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Pro Phe Glu Cys Asn Met Cys Gly Tyr Arg Ser His Asp Arg Tyr Glu
480 485 490

5 TTC TCC TCT CAC ATC GCC AGA GGA GAG CAC AGA GCC ATG TTG AAG T
1895

Phe Ser Ser His Ile Ala Arg Gly Glu His Arg Ala Met Leu Lys
495 500 505

10 GAGCATCTGT CCTCAATGCG AGGGTCAACA TTGTTTTTTA AAGCTGATGG TAGCCTTATC
1955

CAGTAGACTG AACTCAAACC CACCTCGAG
1984

15 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 507 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

25 Met Glu Asp Ile Gln Pro Thr Val Glu Leu Lys Ser Thr Glu Glu Gln
1 5 10 15

30 Pro Leu Pro Thr Glu Ser Pro Asp Ala Leu Asn Asp Tyr Ser Leu Pro
20 25 30

Lys Pro His Glu Ile Glu Asn Val Asp Ser Arg Glu Ala Pro Ala Asn
35 35 40 45

35 Glu Asp Glu Asp Ala Gly Glu Asp Ser Met Lys Val Lys Asp Glu Tyr
50 55 60

Ser Asp Arg Asp Glu Asn Ile Met Lys Pro Glu Pro Met Gly Asp Ala
40 65 70 75 80

Glu Glu Ser Glu Met Pro Tyr Ser Tyr Ala Arg Glu Tyr Ser Asp Tyr
85 90 95

45 Glu Ser Ile Lys Leu Glu Arg His Val Pro Tyr Asp Asn Ser Arg Pro
100 105 110

Thr Ser Gly Lys Met Asn Cys Asp Val Cys Gly Leu Ser Cys Ile Ser
115 120 125

50 Phe Asn Val Leu Met Val His Lys Arg Ser His Thr Gly Glu Arg Pro
130 135 140

Phe Gln Cys Asn Gln Cys Gly Ala Ser Phe Thr Gln Lys Gly Asn Leu
145 150 155 160

55 Leu Arg His Ile Lys Leu His Thr Gly Glu Lys Pro Phe Lys Cys His
165 170 175

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Leu Cys Asn Tyr Ala Cys Gln Arg Arg Asp Ala Leu Thr Gly His Leu
180 185 190

5 Arg Thr His Ser Val Glu Lys Pro Tyr Lys Cys Glu Phe Cys Gly Arg
195 200 205

Ser Tyr Lys Gln Arg Ser Ser Leu Glu Glu His Lys Glu Arg Cys Arg
210 215 220

10 Ala Phe Leu Gln Asn Pro Asp Leu Gly Asp Ala Ala Ser Val Glu Ala
225 230 235 240

Arg His Ile Lys Ala Glu Met Gly Ser Glu Arg Ala Leu Val Leu Asp
15 245 250 255

Arg Leu Ala Ser Asn Val Ala Lys Arg Lys Ser Ser Met Pro Gln Lys
260 265 270

20 Phe Ile Gly Glu Lys Arg His Cys Phe Asp Ala Asn Tyr Asn Pro Gly
275 280 285

Tyr Met Tyr Glu Lys Glu Asn Glu Met Met Gln Thr Arg Met Met Asp
290 295 300

25 Gln Ala Ile Asn Asn Ala Ile Ser Tyr Leu Gly Ala Glu Ala Phe Arg
305 310 315 320

Pro Leu Val Gln Thr Pro Pro Ala Pro Thr Ser Glu Met Val Pro Val
30 325 330 335

Ile Ser Ser Val Tyr Pro Ile Ala Leu Thr Arg Ala Asp Met Pro Met
340 345 350

35 Gly Ala Pro Gln Glu Met Glu Lys Lys Arg Ile Leu Leu Pro Glu Lys
355 360 365

Ile Leu Pro Ser Glu Arg Gly Leu Ser Pro Asn Asn Ser Ala Gln Asp
370 375 380

40 Ser Thr Asp Thr Asp Ser Asn His Glu Asp Arg Gln His Leu Tyr Gln
385 390 395 400

Gln Ser His Val Val Leu Pro Gln Ala Arg Asn Gly Met Pro Leu Leu
45 405 410 415

Lys Glu Val Pro Arg Ser Phe Glu Leu Leu Lys Pro Pro Pro Ile Cys
420 425 430

50 Leu Arg Asp Ser Ile Lys Val Ile Asn Lys Glu Gly Glu Val Met Asp
435 440 445

Val Phe Arg Cys Asp His Cys His Val Leu Phe Leu Asp Tyr Val Met
450 455 460

55 Phe Thr Ile His Met Gly Cys His Gly Phe Arg Asp Pro Phe Glu Cys
465 470 475 480

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Asn Met Cys Gly Tyr Arg Ser His Asp Arg Tyr Glu Phe Ser Ser His
485 490 495

5 Ile Ala Arg Gly Glu His Arg Ala Met Leu Lys
500 505

(2) INFORMATION FOR SEQ ID NO:3:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TACTACCATC TCACATGGGC TGACCA
26

25 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GACCAGCACA TGTGACACT CTGAAA
40 26

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
45 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

55 GTGTGCGGGT TATCCTGCAT TAGC
24

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865020.846T060

(2) INFORMATION FOR SEQ ID NO:6:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATCGAAGCAG TGCCGCTTCT CACC
24

20 (2) INFORMATION FOR SEQ ID NO:7:

(2) INFORMATION FOR SEQ ID NO:8:

(2) INFORMATION FOR SEQ ID NO:9:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: cDNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTAACCTCCT CCGTCATATT AAAC
24

40 (2) INFORMATION FOR SEQ ID NO:10:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

55 CGAGCTTTTC TTCAGAACCC TGAC
24

(2) INFORMATION FOR SEQ ID NO:11:

09019348 020598
865020 84E6T060

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCAGCTTTTG GGAATACCCT GTCA

24

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCAGCTTTTG GGGGTACCCT GTCA

24

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGGTGAAGG TCGGTGTGAA CGGATTTGGC

30

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCATCGAAGG TGGAAGAGTG GGAGTTGCTG
30

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 1788 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

25

- (A) NAME/KEY: CDS
- (B) LOCATION: 223..1515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

30

AATTCGTTCT ACCTTCTCTG AACCCAGTG GTGTGTCAAG GCCGGACTGG GAGCTTGGGG 60

GAAGAGGAAG AGGAAGAGGA ATCTGCGGCT CATCCAGGGA TCAGGGTCCT TCCCAAGTGG 120

CCACTCAGAG GGGACTCAGA GCAAGTCTAG ATTTGTGTGG CAGAGAGAGA CAGCTCTCGT 180

35

TTGGCCTTGG GGAGGCACAA GTCTGTTGAT AACCTGAAGA CA 222

ATG GAT GTC GAT GAG GGT CAA GAC ATG TCC CAA GTT TCA GGA AAG GAG 270
Met Asp Val Asp Glu Gly Gln Asp Met Ser Gln Val Ser Gly Lys Glu
1 5 10 15

40

AGC CCC CCA GTC AGT GAC ACT CCA GAT GAA GGG GAT GAG CCC ATG CCT 318
Ser Pro Pro Val Ser Asp Thr Pro Asp Glu Gly Asp Glu Pro Met Pro
20 25 30

45

GTC CCT GAG GAC CTG TCC ACT ACC TCT GGA GCA CAG CAG AAC TCC AAG 366
Val Pro Glu Asp Leu Ser Thr Thr Ser Gly Ala Gln Gln Asn Ser Lys
35 40 45

50

AGT GAT CGA GGC ATG GGT GAA CGG CCT TTC CAG TGC AAC CAG TCT GGG 414
Ser Asp Arg Gly Met Gly Gln Arg Pro Phe Gln Cys Asn Gln Ser Gly
50 55 60

55

GCC TCC TTT ACC CAG AAA GGC AAC CTC CTG CGG CAC ATC AAG CTG CAC 462
Ala Ser Phe Thr Gln Lys Gly Asn Leu Leu Arg His Ile Lys Leu His
65 70 75 80

TCG GGT GAG AAG CCC TTC AAA TGC CAT CTT TGC AAC TAT GCC TGC CGC 510

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	Ser	Gly	Glu	Lys	Pro	Phe	Lys	Cys	His	Leu	Cys	Asn	Tyr	Ala	Cys	Arg	
					85					90					95		
5	CGG	AGG	GAC	GCC	CTC	ACC	GGC	CAC	CTG	AGG	ACG	CAC	TCC	GTT	GGT	AAG	558
	Arg	Arg	Asp	Ala	Leu	Thr	Gly	His	Leu	Arg	Thr	His	Ser	Val	Gly	Lys	
				100				105					110				
10	CCT	CAC	AAA	TGT	GGA	TAT	TGT	GGC	CGG	AGC	TAT	AAA	CAG	CGA	AGC	TCT	606
	Pro	His	Lys	Cys	Gly	Tyr	Cys	Gly	Arg	Ser	Tyr	Lys	Gln	Arg	Ser	Ser	
			115					120					125				
15	TTA	GAG	GAG	CAT	AAA	GAG	CGA	TGC	CAC	AAC	TAC	TTG	GAA	AGC	ATG	GGC	654
	Leu	Glu	Glu	His	Lys	Glu	Arg	Cys	His	Asn	Tyr	Leu	Glu	Ser	Met	Gly	
		130					135					140					
20	CTT	CCG	GGC	GTG	TGC	CCA	GTC	ATT	AAG	GAA	GAA	ACT	AAC	CAC	AAC	GAG	702
	Leu	Pro	Gly	Val	Cys	Pro	Val	Ile	Lys	Glu	Glu	Thr	Asn	His	Asn	Glu	
		145				150					155					160	
25	ATG	GCA	GAA	GAC	CTG	TGC	AAG	ATA	GGA	GCA	GAG	AGG	TCC	CTT	GTC	CTG	750
	Met	Ala	Glu	Asp	Leu	Cys	Lys	Ile	Gly	Ala	Glu	Arg	Ser	Leu	Val	Leu	
					165				170						175		
30	GAC	AGG	CTG	GCA	AGC	AAT	GTC	GCC	AAA	CGT	AAG	AGC	TCT	ATG	CCT	CAG	798
	Asp	Arg	Leu	Ala	Ser	Asn	Val	Ala	Lys	Arg	Lys	Ser	Ser	Met	Pro	Gln	
				180				185						190			
35	AAA	TTT	CTT	GGA	GAC	AAG	TGC	CTG	TCA	GAC	ATG	CCC	TAT	GAC	AGT	GCC	846
	Lys	Phe	Leu	Gly	Asp	Lys	Cys	Leu	Ser	Asp	Met	Pro	Tyr	Asp	Ser	Ala	
			195				200						205				
40	AAC	TAT	GAG	AAG	GAG	GAT	ATG	ATG	ACA	TCC	CAC	GTG	ATG	GAC	CAG	GCC	894
	Asn	Tyr	Glu	Lys	Glu	Asp	Met	Met	Thr	Ser	His	Val	Met	Asp	Gln	Ala	
		210				215						220					
45	ATC	AAC	AAT	GCC	ATC	AAC	TAC	CTG	GGG	GCT	GAG	TCC	CTG	CGC	CCA	TTG	942
	Ile	Asn	Asn	Ala	Ile	Asn	Tyr	Leu	Gly	Ala	Glu	Ser	Leu	Arg	Pro	Leu	
		225				230					235					240	
50	GTG	CAG	ACA	CCC	CCC	GGT	AGC	TCC	GAG	GTG	GTG	CCA	GTC	ATC	AGC	TCC	990
	Val	Gln	Thr	Pro	Pro	Gly	Ser	Ser	Glu	Val	Val	Pro	Val	Ile	Ser	Ser	
				245					250						255		
55	ATG	TAC	CAG	CTG	CAC	AAG	CCC	CCC	TCA	GAT	GGC	CCC	CCA	CGG	TCC	AAC	1038
	Met	Tyr	Gln	Leu	His	Lys	Pro	Pro	Ser	Asp	Gly	Pro	Pro	Arg	Ser	Asn	
				260				265					270				
60	CAT	TCA	GCA	CAG	GAC	GCC	GTG	GAT	AAC	TTG	CTG	CTG	CTG	TCC	AAG	GCC	1086
	His	Ser	Ala	Gln	Asp	Ala	Val	Asp	Asn	Leu	Leu	Leu	Leu	Ser	Lys	Ala	
			275				280					285					
65	AAG	TCT	GTG	TCA	TCG	GAG	CGA	GAG	GCC	TCC	CCG	AGC	AAC	AGC	TGC	CAA	1134
	Lys	Ser	Val	Ser	Ser	Glu	Arg	Glu	Ala	Ser	Pro	Ser	Asn	Ser	Cys	Gln	
		290				295					300						
70	GAC	TCC	ACA	GAT	ACA	GAG	AGC	AAC	GCG	GAG	GAA	CAG	CGC	AGC	GGC	CTT	1182
	Asp	Ser	Thr	Asp	Thr	Glu	Ser	Asn	Ala	Glu	Glu	Gln	Arg	Ser	Gly	Leu	

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	305		310		315		320	
	ATC	TAC	CTA	ACC	AAC	CAC	ATC	AAC
	Ile	Tyr	Leu	Thr	Asn	His	Ile	Asn
5					325			330
	CTC	AAG	GAG	GAG	CAG	CGC	GCC	TAC
	Leu	Lys	Glu	Glu	Gln	Arg	Ala	Tyr
10				340			345	
	AAC	TCG	CAG	GAT	GCC	TTC	CGT	GTG
	Asn	Ser	Gln	Asp	Ala	Phe	Arg	Val
			355				360	
15	AAG	GTG	TAC	AAG	TGC	GAA	CAC	TGC
	Lys	Val	Tyr	Lys	Cys	Glu	His	Cys
			370				375	
20	ATG	TAT	ACC	ATT	CAC	ATG	GGC	TGC
	Met	Tyr	Thr	Ile	His	Met	Gly	Cys
			385			390		395
	CCC	TTT	GAG	TGT	AAC	ATG	TGT	GGT
25	Pro	Phe	Glu	Cys	Asn	Met	Cys	Gly
				405			410	
	TTC	TCA	TCC	CAT	ATC	ACG	CGG	GGG
	Phe	Ser	Ser	His	Ile	Thr	Arg	Gly
30				420			425	
	TAA	ACC	CAG	C	AGG	CCCC	CAC	TGA
								AAG
								CACAA
								AGATAGCTGG
								TTATGCCTCC
								TTCCC
								GGCAG
35	GGT	TG	TTT	TGG	CGT	TT	CATT	T
								GC
								CG
								TTGGAAG
								ATAAGTTTTT
								AATGTTAGTG
								ACAGGATTGC
								1695
	ATT	GC	AT	CAG	CA	AC	AT	T
								CAC
								AACATCCATC
								CTTCTAGCCA
								GTTTTGTTCA
								CTGGTAGCTG
								1755
40	AGG	TTT	CCCC	G	AT	T	G	T
								GGC
								TTC
								CTA
								AC
								AC
								TCT
								1788

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

09019348.020598

	AAT GTT AAA GTA GAG ACT CAG AGT GAT GAA GAG AAT GGG CGT GCC TGT	
	48	
5	Asn Val Lys Val Glu Thr Gln Ser Asp Glu Glu Asn Gly Arg Ala Cys	
	1 5 10 15	
	GAA ATG AAT GGG GAA GAA TGT GCG GAG GAT TTA CGA ATG CTT GAT GCC	
	96	
10	Glu Met Asn Gly Glu Glu Cys Ala Glu Asp Leu Arg Met Leu Asp Ala	
	20 25 30	
	TCG GGA GAG AAA ATG AAT GGC TCC CAC AGG GAC CAA GGC AGC TCG GCT	
	144	
15	Ser Gly Glu Lys Met Asn Gly Ser His Arg Asp Gln Gly Ser Ser Ala	
	35 40 45	
	TTG TCG GGA GTT GGA GGC ATT CGA CTT CCT AAC GGA AAA CTA AAG TGT	
	192	
20	Leu Ser Gly Val Gly Gly Ile Arg Leu Pro Asn Gly Lys Leu Lys Cys	
	50 55 60	
	GAT ATC TGT GGG ATC ATT TGC ATC GGG CCC AAT GTG CTC ATG GTT CAC	
	240	
25	Asp Ile Cys Gly Ile Ile Cys Ile Gly Pro Asn Val Leu Met Val His	
	65 70 75 80	
	AAA AGA AGC CAC ACT GGA GAA CGG CCC TTC CAG TGC AAT CAG TGC GGG	
	288	
30	Lys Arg Ser His Thr Gly Glu Arg Pro Phe Gln Cys Asn Gln Cys Gly	
	85 90 95	
	GCC TCA TTC ACC CAG AAG GGC AAC CTG CTC CGG CAC ATC AAG CTG CAT	
	336	
35	Ala Ser Phe Thr Gln Lys Gly Asn Leu Leu Arg His Ile Lys Leu His	
	100 105 110	
	TCC GGG GAG AAG CCC TTC AAA TGC CAC CTC TGC AAC TAC GCC TGC CGC	
	384	
40	Ser Gly Glu Lys Pro Phe Lys Cys His Leu Cys Asn Tyr Ala Cys Arg	
	115 120 125	
	CGG AGG GAC GCC CTC ACT GGC CAC CTG AGG ACG CAC TCC GTT GGT AAA	
	432	
45	Arg Arg Asp Ala Leu Thr Gly His Leu Arg Thr His Ser Val Gly Lys	
	130 135 140	
	CCT CAC AAA TGT GGA TAT TGT GGC CGA AGC TAT AAA CAG CGA ACG TCT	
	480	
50	Pro His Lys Cys Gly Tyr Cys Gly Arg Ser Tyr Lys Gln Arg Thr Ser	
	145 150 155 160	
	TTA GAG GAA CAT AAA GAG CGC TGC CAC AAC TAC TTG GAA AGC ATG GGC	
	528	
55	Leu Glu Glu His Lys Glu Arg Cys His Asn Tyr Leu Glu Ser Met Gly	
	165 170 175	

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CTT CCG GGC ACA CTG TAC CCA GTC ATT AAA GAA GAA ACT AAG CAC AGT
576
Leu Pro Gly Thr Leu Tyr Pro Val Ile Lys Glu Glu Thr Lys His Ser
180 185 190

5
GAA ATG GCA GAA GAC CTG TGC AAG ATA GGA TCA GAG AGA TCT CTC GTG
624
Glu Met Ala Glu Asp Leu Cys Lys Ile Gly Ser Glu Arg Ser Leu Val
195 200 205

10
CTG GAC AGA CTA GCA AGT AAT GTC GCC AAA CGT AAG AGC TCT ATG CCT
672
Leu Asp Arg Leu Ala Ser Asn Val Ala Lys Arg Lys Ser Ser Met Pro
210 215 220

15
CAG AAA TTT CTT GGG GAC AAG GGC CTG TCC GAC ACG CCC TAC GAC AGT
720
Gln Lys Phe Leu Gly Asp Lys Gly Leu Ser Asp Thr Pro Tyr Asp Ser
225 230 235 240

20
GCC ACG TAC GAG AAG GAG AAC GAA ATG ATG AAG TCC CAC GTG ATG GAC
768
Ala Thr Tyr Glu Lys Glu Asn Glu Met Met Lys Ser His Val Met Asp
245 250 255

25
CAA GCC ATC AAC AAC GCC ATC AAC TAC CTG GGG GCC GAG TCC CTG CGC
816
Gln Ala Ile Asn Asn Ala Ile Asn Tyr Leu Gly Ala Glu Ser Leu Arg
260 265 270

30
CCG CTG GTG CAG ACG CCC CCG GGC GGT TCC GAG GTG GTC CCG GTC ATC
864
Pro Leu Val Gln Thr Pro Pro Gly Gly Ser Glu Val Val Pro Val Ile
275 280 285

35
AGC CCG ATG TAC CAG CTG CAC AGG CGC TCG GAG GGC ACC CCG CGC TCC
912
Ser Pro Met Tyr Gln Leu His Arg Arg Ser Glu Gly Thr Pro Arg Ser
290 295 300

40
AAC CAC TCG GCC CAG GAC AGC GCC GTG GAG TAC CTG CTG CTG CTC TCC
960
Asn His Ser Ala Gln Asp Ser Ala Val Glu Tyr Leu Leu Leu Leu Ser
305 310 315 320

45
AAG GCC AAG TTG GTG CCC TCG GAG CGC GAG GCG TCC CCG AGC AAC AGC
1008
Lys Ala Lys Leu Val Pro Ser Glu Arg Glu Ala Ser Pro Ser Asn Ser
325 330 335

50
TGC CAA GAC TCC ACG GAC ACC GAG AGC AAC AAC GAG GAG CAG CGC AGC
1056
Cys Gln Asp Ser Thr Asp Thr Glu Ser Asn Asn Glu Glu Gln Arg Ser
340 345 350

55
GGT CTT ATC TAC CTG ACC AAC CAC ATC GCC CGA CGC GCG CAA CGC GTG
1104

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Gly Leu Ile Tyr Leu Thr Asn His Ile Ala Arg Arg Ala Gln Arg Val
355 360 365

5 TCG CTC AAG GAG GAG CAC CGC GCC TAC GAC CTG CTG CGC GCC GCC TCC
1152

Ser Leu Lys Glu Glu His Arg Ala Tyr Asp Leu Leu Arg Ala Ala Ser
370 375 380

10 GAG AAC TCG CAG GAC GCG CTC CGC GTG GTC AGC ACC AGC GGG GAG CAG
1200

Glu Asn Ser Gln Asp Ala Leu Arg Val Val Ser Thr Ser Gly Glu Gln
385 390 395 400

15 ATG AAG GTG TAC AAG TGC GAA CAC TGC CGG GTG CTC TTC CTG GAT CAC
1248

Met Lys Val Tyr Lys Cys Glu His Cys Arg Val Leu Phe Leu Asp His
405 410 415

20 GTC ATG TAC ACC ATC CAC ATG GGC TGC CAC GGC TTC CGT GAT CCT TTT
1296

Val Met Tyr Thr Ile His Met Gly Cys His Gly Phe Arg Asp Pro Phe
420 425 430

25 GAG TGC AAC ATG TGC GGC TAC CAC AGC CAG GAC CGG TAC GAG TTC TCG
1344

Glu Cys Asn Met Cys Gly Tyr His Ser Gln Asp Arg Tyr Glu Phe Ser
435 440 445

30 TCG CAC ATA ACG CGA GGG GAG CAC CGC TTC CAC ATG AGC TAA
1386

Ser His Ile Thr Arg Gly Glu His Arg Phe His Met Ser
450 455 460

(2) INFORMATION FOR SEQ ID NO:17:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1296 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

45 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1296

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATG GAT GTC GAT GAG GGT CAA GAC ATG TCC CAA GTT TCA GGA AAG GAG
48

55 Met Asp Val Asp Glu Gly Gln Asp Met Ser Gln Val Ser Gly Lys Glu
1 5 10 15

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AGC CCC CCA GTC AGT GAC ACT CCA GAT GAA GGG GAT GAG CCC ATG CCT
96
Ser Pro Pro Val Ser Asp Thr Pro Asp Glu Gly Asp Glu Pro Met Pro
20 25 30

5 GTC CCT GAG GAC CTG TCC ACT ACC TCT GGA GCA CAG CAG AAC TCC AAG
144
Val Pro Glu Asp Leu Ser Thr Thr Ser Gly Ala Gln Gln Asn Ser Lys
35 40 45

10 AGT GAT CGA GGC ATG GCC AGT AAT GTT AAA GTA GAG ACT CAG AGT GAT
192
Ser Asp Arg Gly Met Ala Ser Asn Val Lys Val Glu Thr Gln Ser Asp
50 55 60

15 GAA GAG AAT GGG CGT GCC TGT GAA ATG AAT GGG GAA GAA TGT GCA GAG
240
Glu Glu Asn Gly Arg Ala Cys Glu Met Asn Gly Glu Glu Cys Ala Glu
65 70 75 80

20 GAT TTA CGA ATG CTT GAT GCC TCG GGA GAG AAA ATG AAT GGC TCC CAC
288
Asp Leu Arg Met Leu Asp Ala Ser Gly Glu Lys Met Asn Gly Ser His
85 90 95

25 AGG GAC CAA GGC AGC TCG GCT TTG TCA GGA GTT GGA GGC ATT CGA CTT
336
Arg Asp Gln Gly Ser Ser Ala Leu Ser Gly Val Gly Gly Ile Arg Leu
100 105 110

30 CCT AAC GGA AAA CTA AAG TGT GAT ATC TGT GGG ATC GTT TGC ATC GGG
384
Pro Asn Gly Lys Leu Lys Cys Asp Ile Cys Gly Ile Val Cys Ile Gly
115 120 125

35 CCC AAT GTG CTC ATG GTT CAC AAA AGA AGT CAT ACT GGT GAA CGG CCT
432
Pro Asn Val Leu Met Val His Lys Arg Ser His Thr Gly Glu Arg Pro
130 135 140

40 TTC CAG TGC AAC CAG TCT GGG GCC TCC TTT ACC CAG AAA GGC AAC CTC
480
Phe Gln Cys Asn Gln Ser Gly Ala Ser Phe Thr Gln Lys Gly Asn Leu
145 150 155 160

45 CTG CGG CAC ATC AAG CTG CAC TCG GGT GAG AAG CCC TTC AAA TGC CAT
528
Leu Arg His Ile Lys Leu His Ser Gly Glu Lys Pro Phe Lys Cys His
165 170 175

50 CTT TGC AAC TAT GCC TGC CGC CGG AGG GAC GCC CTC ACC GGC CAC CTG
576
Leu Cys Asn Tyr Ala Cys Arg Arg Arg Asp Ala Leu Thr Gly His Leu
180 185 190

55 AGG ACG CAC TCC GGA GAC AAG TGC CTG TCA GAC ATG CCC TAT GAC AGT
624

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	Arg	Thr	His	Ser	Gly	Asp	Lys	Cys	Leu	Ser	Asp	Met	Pro	Tyr	Asp	Ser
			195					200					205			
5	GCC	AAC	TAT	GAG	AAG	GAG	GAT	ATG	ATG	ACA	TCC	CAC	GTG	ATG	GAC	CAG
	672															
	Ala	Asn	Tyr	Glu	Lys	Glu	Asp	Met	Met	Thr	Ser	His	Val	Met	Asp	Gln
	210						215					220				
10	GCC	ATC	AAC	AAT	GCC	ATC	AAC	TAC	CTG	GGG	GCT	GAG	TCC	CTG	CGC	CCA
	720															
	Ala	Ile	Asn	Asn	Ala	Ile	Asn	Tyr	Leu	Gly	Ala	Glu	Ser	Leu	Arg	Pro
	225					230					235					240
15	TTG	GTG	CAG	ACA	CCC	CCC	GGT	AGC	TCC	GAG	GTG	GTG	CCA	GTC	ATC	AGC
	768															
	Leu	Val	Gln	Thr	Pro	Pro	Gly	Ser	Ser	Glu	Val	Val	Pro	Val	Ile	Ser
					245					250					255	
20	TCC	ATG	TAC	CAG	CTG	CAC	AAG	CCC	CCC	TCA	GAT	GGC	CCC	CCA	CGG	TCC
	816															
	Ser	Met	Tyr	Gln	Leu	His	Lys	Pro	Pro	Ser	Asp	Gly	Pro	Pro	Arg	Ser
				260					265					270		
25	AAC	CAT	TCA	GCA	CAG	GAC	GCC	GTG	GAT	AAC	TTG	CTG	CTG	CTG	TCC	AAG
	864															
	Asn	His	Ser	Ala	Gln	Asp	Ala	Val	Asp	Asn	Leu	Leu	Leu	Leu	Ser	Lys
			275					280					285			
30	GCC	AAG	TCT	GTG	TCA	TCG	GAG	CGA	GAG	GCC	TCC	CCG	AGC	AAC	AGC	TGC
	912															
	Ala	Lys	Ser	Val	Ser	Ser	Glu	Arg	Glu	Ala	Ser	Pro	Ser	Asn	Ser	Cys
		290					295					300				
35	CAA	GAC	TCC	ACA	GAT	ACA	GAG	AGC	AAC	GCG	GAG	GAA	CAG	CGC	AGC	GGC
	960															
	Gln	Asp	Ser	Thr	Asp	Thr	Glu	Ser	Asn	Ala	Glu	Glu	Gln	Arg	Ser	Gly
	305					310					315					320
40	CTT	ATC	TAC	CTA	ACC	AAC	CAC	ATC	AAC	CCG	CAT	GCA	CGC	AAT	GGG	CTG
	1008															
	Leu	Ile	Tyr	Leu	Thr	Asn	His	Ile	Asn	Pro	His	Ala	Arg	Asn	Gly	Leu
					325					330					335	
45	GCT	CTC	AAG	GAG	GAG	CAG	CGC	GCC	TAC	GAG	GTG	CTG	AGG	GCG	GCC	TCA
	1056															
	Ala	Leu	Lys	Glu	Glu	Gln	Arg	Ala	Tyr	Glu	Val	Leu	Arg	Ala	Ala	Ser
				340					345					350		
50	GAG	AAC	TCG	CAG	GAT	GCC	TTC	CGT	GTG	GTC	AGC	ACG	AGT	GGC	GAG	CAG
	1104															
	Glu	Asn	Ser	Gln	Asp	Ala	Phe	Arg	Val	Val	Ser	Thr	Ser	Gly	Glu	Gln
			355					360					365			
55	CTG	AAG	GTG	TAC	AAG	TGC	GAA	CAC	TGC	CGC	GTG	CTC	TTC	CTG	GAT	CAC
	1152															
	Leu	Lys	Val	Tyr	Lys	Cys	Glu	His	Cys	Arg	Val	Leu	Phe	Leu	Asp	His
		370					375					380				

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GTC ATG TAT ACC ATT CAC ATG GGC TGC CAT GGC TGC CAT GGC TTT CGG
1200
Val Met Tyr Thr Ile His Met Gly Cys His Gly Cys His Gly Phe Arg
5 385 390 395 400

GAT CCC TTT GAG TGT AAC ATG TGT GGT TAT CAC AGC CAG GAC AGG TAC
1248
Asp Pro Phe Glu Cys Asn Met Cys Gly Tyr His Ser Gln Asp Arg Tyr
10 405 410 415

GAG TTC TCA TCC CAT ATC ACG CGG GGG GAG CAT CGT TAC CAC CTG AGC
1296
Glu Phe Ser Ser His Ile Thr Arg Gly Glu His Arg Tyr His Leu Ser
15 420 425 430

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 2049 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
30 (A) NAME/KEY: CDS
(B) LOCATION: 223..1776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

35 AATTCGTTCT ACCTTCTCTG AACCCAGTG GTGTGTCAAG GCCGGACTGG GAGCTTGGGG
60

GAAGAGGAAG AGGAAGAGGA ATCTGCGGCT CATCCAGGGA TCAGGGTCCT TCCCAAGTGG
40 120

CCACTCAGAG GGGACTCAGA GCAAGTCTAG ATTTGTGTGG CAGAGAGAGA CAGCTCTCGT
180

45 TTGGCCTTGG GGAGGCACAA GTCTGTTGAT AACCTGAAGA CA ATG GAT GTC GAT
234

Met Asp Val Asp
1

50 GAG GGT CAA GAC ATG TCC CAA GTT TCA GGA AAG GAG AGC CCC CCA GTC
282
Glu Gly Gln Asp Met Ser Gln Val Ser Gly Lys Glu Ser Pro Pro Val
5 10 15 20

55 AGT GAC ACT CCA GAT GAA GGG GAT GAG CCC ATG CCT GTC CCT GAG GAC
330
Ser Asp Thr Pro Asp Glu Gly Asp Glu Pro Met Pro Val Pro Glu Asp
25 30 35

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	CTG	TCC	ACT	ACC	TCT	GGA	GCA	CAG	CAG	AAC	TCC	AAG	AGT	GAT	CGA	GGC	
	378																
5	Leu	Ser	Thr	Thr	Ser	Gly	Ala	Gln	Gln	Asn	Ser	Lys	Ser	Asp	Arg	Gly	
				40					45					50			
	ATG	GCC	AGT	AAT	GTT	AAA	GTA	GAG	ACT	CAG	AGT	GAT	GAA	GAG	AAT	GGG	
	426																
10	Met	Ala	Ser	Asn	Val	Lys	Val	Glu	Thr	Gln	Ser	Asp	Glu	Glu	Asn	Gly	
			55					60					65				
	CGT	GCC	TGT	GAA	ATG	AAT	GGG	GAA	GAA	TGT	GCA	GAG	GAT	TTA	CGA	ATG	
	474																
15	Arg	Ala	Cys	Glu	Met	Asn	Gly	Glu	Glu	Cys	Ala	Glu	Asp	Leu	Arg	Met	
		70					75					80					
	CTT	GAT	GCC	TCG	GGA	GAG	AAA	ATG	AAT	GGC	TCC	CAC	AGG	GAC	CAA	GGC	
	522																
20	Leu	Asp	Ala	Ser	Gly	Glu	Lys	Met	Asn	Gly	Ser	His	Arg	Asp	Gln	Gly	
	85					90					95				100		
	AGC	TCG	GCT	TTG	TCA	GGA	GTT	GGA	GGC	ATT	CGA	CTT	CCT	AAC	GGA	AAA	
	570																
25	Ser	Ser	Ala	Leu	Ser	Gly	Val	Gly	Gly	Ile	Arg	Leu	Pro	Asn	Gly	Lys	
					105					110					115		
	CTA	AAG	TGT	GAT	ATC	TGT	GGG	ATC	GTT	TGC	ATC	GGG	CCC	AAT	GTG	CTC	
	618																
30	Leu	Lys	Cys	Asp	Ile	Cys	Gly	Ile	Val	Cys	Ile	Gly	Pro	Asn	Val	Leu	
				120					125					130			
	ATG	GTT	CAC	AAA	AGA	AGT	CAT	ACT	GGT	GAA	CGG	CCT	TTC	CAG	TGC	AAC	
	666																
35	Met	Val	His	Lys	Arg	Ser	His	Thr	Gly	Glu	Arg	Pro	Phe	Gln	Cys	Asn	
			135					140					145				
	CAG	TCT	GGG	GCC	TCC	TTT	ACC	CAG	AAA	GGC	AAC	CTC	CTG	CGG	CAC	ATC	
	714																
40	Gln	Ser	Gly	Ala	Ser	Phe	Thr	Gln	Lys	Gly	Asn	Leu	Leu	Arg	His	Ile	
		150					155					160					
	AAG	CTG	CAC	TCG	GGT	GAG	AAG	CCC	TTC	AAA	TGC	CAT	CTT	TGC	AAC	TAT	
	762																
45	Lys	Leu	His	Ser	Gly	Glu	Lys	Pro	Phe	Lys	Cys	His	Leu	Cys	Asn	Tyr	
	165					170					175				180		
	GCC	TGC	CGC	CGG	AGG	GAC	GCC	CTC	ACC	GGC	CAC	CTG	AGG	ACG	CAC	TCC	
	810																
50	Ala	Cys	Arg	Arg	Arg	Asp	Ala	Leu	Thr	Gly	His	Leu	Arg	Thr	His	Ser	
					185					190					195		
	GTT	GGT	AAG	CCT	CAC	AAA	TGT	GGA	TAT	TGT	GGC	CGG	AGC	TAT	AAA	CAG	
	858																
55	Val	Gly	Lys	Pro	His	Lys	Cys	Gly	Tyr	Cys	Gly	Arg	Ser	Tyr	Lys	Gln	
				200					205					210			

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CGA AGC TCT TTA GAG GAG CAT AAA GAG CGA TGC CAC AAC TAC TTG GAA
906
Arg Ser Ser Leu Glu Glu His Lys Glu Arg Cys His Asn Tyr Leu Glu
215 220 225

5 AGC ATG GGC CTT CCG GGC GTG TGC CCA GTC ATT AAG GAA GAA ACT AAC
954
Ser Met Gly Leu Pro Gly Val Cys Pro Val Ile Lys Glu Glu Thr Asn
230 235 240

10 CAC AAC GAG ATG GCA GAA GAC CTG TGC AAG ATA GGA GCA GAG AGG TCC
1002
His Asn Glu Met Ala Glu Asp Leu Cys Lys Ile Gly Ala Glu Arg Ser
245 250 255 260

15 CTT GTC CTG GAC AGG CTG GCA AGC AAT GTC GCC AAA CGT AAG AGC TCT
1050
Leu Val Leu Asp Arg Leu Ala Ser Asn Val Ala Lys Arg Lys Ser Ser
265 270 275

20 ATG CCT CAG AAA TTT CTT GGA GAC AAG TGC CTG TCA GAC ATG CCC TAT
1098
Met Pro Gln Lys Phe Leu Gly Asp Lys Cys Leu Ser Asp Met Pro Tyr
280 285 290

25 GAC AGT GCC AAC TAT GAG AAG GAG GAT ATG ATG ACA TCC CAC GTG ATG
1146
Asp Ser Ala Asn Tyr Glu Lys Glu Asp Met Met Thr Ser His Val Met
295 300 305

30 GAC CAG GCC ATC AAC AAT GCC ATC AAC TAC CTG GGG GCT GAG TCC CTG
1194
Asp Gln Ala Ile Asn Asn Ala Ile Asn Tyr Leu Gly Ala Glu Ser Leu
310 315 320

35 CGC CCA TTG GTG CAG ACA CCC CCC GGT AGC TCC GAG GTG GTG CCA GTC
1242
Arg Pro Leu Val Gln Thr Pro Pro Gly Ser Ser Glu Val Val Pro Val
325 330 335 340

40 ATC AGC TCC ATG TAC CAG CTG CAC AAG CCC CCC TCA GAT GGC CCC CCA
1290
Ile Ser Ser Met Tyr Gln Leu His Lys Pro Pro Ser Asp Gly Pro Pro
345 350 355

45 CGG TCC AAC CAT TCA GCA CAG GAC GCC GTG GAT AAC TTG CTG CTG CTG
1338
Arg Ser Asn His Ser Ala Gln Asp Ala Val Asp Asn Leu Leu Leu Leu
360 365 370

50 TCC AAG GCC AAG TCT GTG TCA TCG GAG CGA GAG GCC TCC CCG AGC AAC
1386
Ser Lys Ala Lys Ser Val Ser Ser Glu Arg Glu Ala Ser Pro Ser Asn
375 380 385

55 AGC TGC CAA GAC TCC ACA GAT ACA GAG AGC AAC GCG GAG GAA CAG CGC
1434

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B65020 SHEET 060

Ser Cys Gln Asp Ser Thr Asp Thr Glu Ser Asn Ala Glu Glu Gln Arg
390 395 400

5 AGC GGC CTT ATC TAC CTA ACC AAC CAC ATC AAC CCG CAT GCA CGC AAT
1482
Ser Gly Leu Ile Tyr Leu Thr Asn His Ile Asn Pro His Ala Arg Asn
405 410 415 420

10 GGG CTG GCT CTC AAG GAG GAG CAG CGC GCC TAC GAG GTG CTG AGG GCG
1530
Gly Leu Ala Leu Lys Glu Glu Gln Arg Ala Tyr Glu Val Leu Arg Ala
425 430 435

15 GCC TCA GAG AAC TCG CAG GAT GCC TTC CGT GTG GTC AGC ACG AGT GGC
1578
Ala Ser Glu Asn Ser Gln Asp Ala Phe Arg Val Val Ser Thr Ser Gly
440 445 450

20 GAG CAG CTG AAG GTG TAC AAG TGC GAA CAC TGC CGC GTG CTC TTC CTG
1626
Glu Gln Leu Lys Val Tyr Lys Cys Glu His Cys Arg Val Leu Phe Leu
455 460 465

25 GAT CAC GTC ATG TAT ACC ATT CAC ATG GGC TGC CAT GGC TGC CAT GGC
1674
Asp His Val Met Tyr Thr Ile His Met Gly Cys His Gly Cys His Gly
470 475 480

30 TTT CGG GAT CCC TTT GAG TGT AAC ATG TGT GGT TAT CAC AGC CAG GAC
1722
Phe Arg Asp Pro Phe Glu Cys Asn Met Cys Gly Tyr His Ser Gln Asp
485 490 495 500

35 AGG TAC GAG TTC TCA TCC CAT ATC ACG CGG GGG GAG CAT CGT TAC CAC
1770
Arg Tyr Glu Phe Ser Ser His Ile Thr Arg Gly Glu His Arg Tyr His
505 510 515

40 CTG AGC TAAACCCAGC CAGGCCCCAC TGAAGCACAA AGATAGCTGG TTATGCCTCC
1826
Leu Ser

45 TTCCCGGCAG CTGGACCCAC AGCGGACAAT GTGGGAGTGG ATTTGCAGGC AGCATTGTGT
1886
CTTTTATGTT GGTGTGTTTGG CGTTTCATTT GCGTTGGAAG ATAAGTTTTT AATGTTAGTG
1946

50 ACAGGATTGC ATTGCATCAG CAACATTCAC AACATCCATC CTTCTAGCCA GTTTTGTTC
2006
CTGGTAGCTG AGGTTTCCCG GATATGTGGC TTCCTAACAC TCT
2049

55 (2) INFORMATION FOR SEQ ID NO:19:

09019348.020599

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1170 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG GAT GTC GAT GAG GGT CAA GAC ATG TCC CAA GTT TCA GGA AAG GAG
 48
 Met Asp Val Asp Glu Gly Gln Asp Met Ser Gln Val Ser Gly Lys Glu
 20 1 5 10 15
 AGC CCC CCA GTC AGT GAC ACT CCA GAT GAA GGG GAT GAG CCC ATG CCT
 96
 Ser Pro Pro Val Ser Asp Thr Pro Asp Glu Gly Asp Glu Pro Met Pro
 25 20 25 30
 GTC CCT GAG GAC CTG TCC ACT ACC TCT GGA GCA CAG CAG AAC TCC AAG
 144
 Val Pro Glu Asp Leu Ser Thr Thr Ser Gly Ala Gln Gln Asn Ser Lys
 30 35 40 45
 AGT GAT CGA GGC ATG GGT GAA CGG CCT TTC CAG TGC AAC CAG TCT GGG
 192
 Ser Asp Arg Gly Met Gly Glu Arg Pro Phe Gln Cys Asn Gln Ser Gly
 35 50 55 60
 GCC TCC TTT ACC CAG AAA GGC AAC CTC CTG CGG CAC ATC AAG CTG CAC
 240
 Ala Ser Phe Thr Gln Lys Gly Asn Leu Leu Arg His Ile Lys Leu His
 40 65 70 75 80
 TCG GGT GAG AAG CCC TTC AAA TGC CAT CTT TGC AAC TAT GCC TGC CGC
 288
 Ser Gly Glu Lys Pro Phe Lys Cys His Leu Cys Asn Tyr Ala Cys Arg
 45 85 90 95
 CGG AGG GAC GCC CTC ACC GGC CAC CTG AGG ACG CAC TCC GTC ATT AAG
 336
 Arg Arg Asp Ala Leu Thr Gly His Leu Arg Thr His Ser Val Ile Lys
 50 100 105 110
 GAA GAA ACT AAC CAC AAC GAG ATG GCA GAA GAC CTG TGC AAG ATA GGA
 384
 Glu Glu Thr Asn His Asn Glu Met Ala Glu Asp Leu Cys Lys Ile Gly
 55 115 120 125

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GCA GAG AGG TCC CTT GTC CTG GAC AGG CTG GCA AGC AAT GTC GCC AAA
 432
 Ala Glu Arg Ser Leu Val Leu Asp Arg Leu Ala Ser Asn Val Ala Lys
 130 135 140
 5
 CGT AAG AGC TCT ATG CCT CAG AAA TTT CTT GGA GAC AAG TGC CTG TCA
 480
 Arg Lys Ser Ser Met Pro Gln Lys Phe Leu Gly Asp Lys Cys Leu Ser
 145 150 155 160
 10
 GAC ATG CCC TAT GAC AGT GCC AAC TAT GAG AAG GAG GAT ATG ATG ACA
 528
 Asp Met Pro Tyr Asp Ser Ala Asn Tyr Glu Lys Glu Asp Met Met Thr
 165 170 175
 15
 TCC CAC GTG ATG GAC CAG GCC ATC AAC AAT GCC ATC AAC TAC CTG GGG
 576
 Ser His Val Met Asp Gln Ala Ile Asn Asn Ala Ile Asn Tyr Leu Gly
 180 185 190
 20
 GCT GAG TCC CTG CGC CCA TTG GTG CAG ACA CCC CCC GGT AGC TCC GAG
 624
 Ala Glu Ser Leu Arg Pro Leu Val Gln Thr Pro Pro Gly Ser Ser Glu
 195 200 205
 25
 GTG GTG CCA GTC ATC AGC TCC ATG TAC CAG CTG CAC AAG CCC CCC TCA
 672
 Val Val Pro Val Ile Ser Ser Met Tyr Gln Leu His Lys Pro Pro Ser
 210 215 220
 30
 GAT GGC CCC CCA CGG TCC AAC CAT TCA GCA CAG GAC GCC GTG GAT AAC
 720
 Asp Gly Pro Pro Arg Ser Asn His Ser Ala Gln Asp Ala Val Asp Asn
 225 230 235 240
 35
 TTG CTG CTG CTG TCC AAG GCC AAG TCT GTG TCA TCG GAG CGA GAG GCC
 768
 Leu Leu Leu Leu Ser Lys Ala Lys Ser Val Ser Ser Glu Arg Glu Ala
 245 250 255
 40
 TCC CCG AGC AAC AGC TGC CAA GAC TCC ACA GAT ACA GAG AGC AAC GCG
 816
 Ser Pro Ser Asn Ser Cys Gln Asp Ser Thr Asp Thr Glu Ser Asn Ala
 260 265 270
 45
 GAG GAA CAG CGC AGC GGC CTT ATC TAC CTA ACC AAC CAC ATC AAC CCG
 864
 Glu Glu Gln Arg Ser Gly Leu Ile Tyr Leu Thr Asn His Ile Asn Pro
 275 280 285
 50
 CAT GCA CGC AAT GGG CTG GCT CTC AAG GAG GAG CAG CGC GCC TAC GAG
 912
 His Ala Arg Asn Gly Leu Ala Leu Lys Glu Glu Gln Arg Ala Tyr Glu
 290 295 300
 55
 GTG CTG AGG GCG GCC TCA GAG AAC TCG CAG GAT GCC TTC CGT GTG GTC
 960

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Val Leu Arg Ala Ala Ser Glu Asn Ser Gln Asp Ala Phe Arg Val Val
305 310 315 320

AGC ACG AGT GGC GAG CAG CTG AAG GTG TAC AAG TGC GAA CAC TGC CGC
5 1008

Ser Thr Ser Gly Glu Gln Leu Lys Val Tyr Lys Cys Glu His Cys Arg
325 330 335

GTG CTC TTC CTG GAT CAC GTC ATG TAT ACC ATT CAC ATG GGC TGC CAT
10 1056

Val Leu Phe Leu Asp His Val Met Tyr Thr Ile His Met Gly Cys His
340 345 350

GGC TGC CAT GGC TTT CGG GAT CCC TTT GAG TGT AAC ATG TGT GGT TAT
15 1104

Gly Cys His Gly Phe Arg Asp Pro Phe Glu Cys Asn Met Cys Gly Tyr
355 360 365

CAC AGC CAG GAC AGG TAC GAG TTC TCA TCC CAT ATC ACG CGG GGG GAG
20 1152

His Ser Gln Asp Arg Tyr Glu Phe Ser Ser His Ile Thr Arg Gly Glu
370 375 380

CAT CGT TAC CAC CTG AGC
25 1170

His Arg Tyr His Leu Ser
385 390

(2) INFORMATION FOR SEQ ID NO:20:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

40 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1128

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATG GAT GTC GAT GAG GGT CAA GAC ATG TCC CAA GTT TCA GGA AAG GAG
48

Met Asp Val Asp Glu Gly Gln Asp Met Ser Gln Val Ser Gly Lys Glu
50 1 5 10 15

AGC CCC CCA GTC AGT GAC ACT CCA GAT GAA GGG GAT GAG CCC ATG CCT
96

Ser Pro Pro Val Ser Asp Thr Pro Asp Glu Gly Asp Glu Pro Met Pro
55 20 25 30

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GTC CCT GAG GAC CTG TCC ACT ACC TCT GGA GCA CAG CAG AAC TCC AAG
 144
 Val Pro Glu Asp Leu Ser Thr Thr Ser Gly Ala Gln Gln Asn Ser Lys
 35 40 45
 5
 AGT GAT CGA GGC ATG GCC AGT AAT GTT AAA GTA GAG ACT CAG AGT GAT
 192
 Ser Asp Arg Gly Met Ala Ser Asn Val Lys Val Glu Thr Gln Ser Asp
 50 55 60
 10
 GAA GAG AAT GGG CGT GCC TGT GAA ATG AAT GGG GAA GAA TGT GCA GAG
 240
 Glu Glu Asn Gly Arg Ala Cys Glu Met Asn Gly Glu Glu Cys Ala Glu
 65 70 75 80
 15
 GAT TTA CGA ATG CTT GAT GCC TCG GGA GAG AAA ATG AAT GGC TCC CAC
 288
 Asp Leu Arg Met Leu Asp Ala Ser Gly Glu Lys Met Asn Gly Ser His
 85 90 95
 20
 AGG GAC CAA GGC AGC TCG GCT TTG TCA GGA GTT GGA GGC ATT CGA CTT
 336
 Arg Asp Gln Gly Ser Ser Ala Leu Ser Gly Val Gly Gly Ile Arg Leu
 100 105 110
 25
 CCT AAC GGA AAA CTA AAG TGT GAT ATC TGT GGG ATC GTT TGC ATC GGG
 384
 Pro Asn Gly Lys Leu Lys Cys Asp Ile Cys Gly Ile Val Cys Ile Gly
 115 120 125
 30
 CCC AAT GTG CTC ATG GTT CAC AAA AGA AGT CAT ACT GGA GAC AAG TGC
 432
 Pro Asn Val Leu Met Val His Lys Arg Ser His Thr Gly Asp Lys Cys
 130 135 140
 35
 CTG TCA GAC ATG CCC TAT GAC AGT GCC AAC TAT GAG AAG GAG GAT ATG
 480
 Leu Ser Asp Met Pro Tyr Asp Ser Ala Asn Tyr Glu Lys Glu Asp Met
 145 150 155 160
 40
 ATG ACA TCC CAC GTG ATG GAC CAG GCC ATC AAC AAT GCC ATC AAC TAC
 528
 Met Thr Ser His Val Met Asp Gln Ala Ile Asn Asn Ala Ile Asn Tyr
 165 170 175
 45
 CTG GGG GCT GAG TCC CTG CGC CCA TTG GTG CAG ACA CCC CCC GGT AGC
 576
 Leu Gly Ala Glu Ser Leu Arg Pro Leu Val Gln Thr Pro Pro Gly Ser
 180 185 190
 50
 TCC GAG GTG GTG CCA GTC ATC AGC TCC ATG TAC CAG CTG CAC AAG CCC
 624
 Ser Glu Val Val Pro Val Ile Ser Ser Met Tyr Gln Leu His Lys Pro
 195 200 205
 55
 CCC TCA GAT GGC CCC CCA CGG TCC AAC CAT TCA GCA CAG GAC GCC GTG
 672

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Pro Ser Asp Gly Pro Pro Arg Ser Asn His Ser Ala Gln Asp Ala Val
210 215 220

5 GAT AAC TTG CTG CTG CTG TCC AAG GCC AAG TCT GTG TCA TCG GAG CGA
720
Asp Asn Leu Leu Leu Leu Ser Lys Ala Lys Ser Val Ser Ser Glu Arg
225 230 235 240

10 GAG GCC TCC CCG AGC AAC AGC TGC CAA GAC TCC ACA GAT ACA GAG AGC
768
Glu Ala Ser Pro Ser Asn Ser Cys Gln Asp Ser Thr Asp Thr Glu Ser
245 250 255

15 AAC GCG GAG GAA CAG CGC AGC GGC CTT ATC TAC CTA ACC AAC CAC ATC
816
Asn Ala Glu Glu Gln Arg Ser Gly Leu Ile Tyr Leu Thr Asn His Ile
260 265 270

20 AAC CCG CAT GCA CGC AAT GGG CTG GCT CTC AAG GAG GAG CAG CGC GCC
864
Asn Pro His Ala Arg Asn Gly Leu Ala Leu Lys Glu Glu Gln Arg Ala
275 280 285

25 TAC GAG GTG CTG AGG GCG GCC TCA GAG AAC TCG CAG GAT GCC TTC CGT
912
Tyr Glu Val Leu Arg Ala Ala Ser Glu Asn Ser Gln Asp Ala Phe Arg
290 295 300

30 GTG GTC AGC ACG AGT GGC GAG CAG CTG AAG GTG TAC AAG TGC GAA CAC
960
Val Val Ser Thr Ser Gly Glu Gln Leu Lys Val Tyr Lys Cys Glu His
305 310 315 320

35 TGC CGC GTG CTC TTC CTG GAT CAC GTC ATG TAT ACC ATT CAC ATG GGC
1008
Cys Arg Val Leu Phe Leu Asp His Val Met Tyr Thr Ile His Met Gly
325 330 335

40 TGC CAT GGC TGC CAT GGC TTT CGG GAT CCC TTT GAG TGT AAC ATG TGT
1056
Cys His Gly Cys His Gly Phe Arg Asp Pro Phe Glu Cys Asn Met Cys
340 345 350

45 GGT TAT CAC AGC CAG GAC AGG TAC GAG TTC TCA TCC CAT ATC ACG CGG
1104
Gly Tyr His Ser Gln Asp Arg Tyr Glu Phe Ser Ser His Ile Thr Arg
355 360 365

50 GGG GAG CAT CGT TAC CAC CTG AGC
1128
Gly Glu His Arg Tyr His Leu Ser
370 375

55 (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1004 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
10 (B) LOCATION: 1..1002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

15 GGA GAA CGG CCC TTC CAG TGC AAT CAG TGC GGG GCC TCA TTC ACC CAG
48
Gly Glu Arg Pro Phe Gln Cys Asn Gln Cys Gly Ala Ser Phe Thr Gln
1 5 10 15

20 AAG GGC AAC CTG CTC CGG CAC ATC AAG CTG CAT TCC GGG GAG AAG CCC
96
Lys Gly Asn Leu Leu Arg His Ile Lys Leu His Ser Gly Glu Lys Pro
20 25 30

25 TTC AAA TGC CAC CTC TGC AAC TAC GCC TGC CGC CGG AGG GAC GCC CTC
144
Phe Lys Cys His Leu Cys Asn Tyr Ala Cys Arg Arg Arg Asp Ala Leu
35 40 45

30 ACT GGC CAC CTG AGG ACG CAC TCC GTC ATT AAA GAA GAA ACT AAG CAC
192
Thr Gly His Leu Arg Thr His Ser Val Ile Lys Glu Glu Thr Lys His
50 55 60

35 AGT GAA ATG GCA GAA GAC CTG TGC AAG ATA GGA TCA GAG AGA TCT CTC
240
Ser Glu Met Ala Glu Asp Leu Cys Lys Ile Gly Ser Glu Arg Ser Leu
65 70 75 80

40 GTG CTG GAC AGA CTA GCA AGT AAT GTC GCC AAA CGT AAG AGC TCT ATG
288
Val Leu Asp Arg Leu Ala Ser Asn Val Ala Lys Arg Lys Ser Ser Met
85 90 95

45 CCT CAG AAA TTT CTT GGG GAC AAG GGC CTG TCC GAC ACG CCC TAC GAC
336
Pro Gln Lys Phe Leu Gly Asp Lys Gly Leu Ser Asp Thr Pro Tyr Asp
100 105 110

50 AGT GCC ACG TAC GAG AAG GAG AAC GAA ATG ATG AAG TCC CAC GTG ATG
384
Ser Ala Thr Tyr Glu Lys Glu Asn Glu Met Met Lys Ser His Val Met
115 120 125

55 GAC CAA GCC ATC AAC AAC GCC ATC AAC TAC CTG GGG GCC GAG TCC CTG
432
Asp Gln Ala Ile Asn Asn Ala Ile Asn Tyr Leu Gly Ala Glu Ser Leu

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	130	135	140
	CGC CCG CTG GTG CAG ACG CCC CCG GGC GGT TCC GAG GTG GTC CCG GTC		
	480		
5	Arg Pro Leu Val Gln Thr Pro Pro Gly Gly Ser Glu Val Val Pro Val	150	155 160
	145		
	ATC AGC CCG ATG TAC CAG CTG CAC AGG CGC TCG GAG GGC ACC CCG CGC		
	528		
10	Ile Ser Pro Met Tyr Gln Leu His Arg Arg Ser Glu Gly Thr Pro Arg	165	170 175
	TCC AAC CAC TCG GCC CAG GAC AGC GCC GTG GAG TAC CTG CTG CTG CTC		
	576		
15	Ser Asn His Ser Ala Gln Asp Ser Ala Val Glu Tyr Leu Leu Leu Leu	180	185 190
	TCC AAG GCC AAG TTG GTG CCC TCG GAG CGC GAG GCG TCC CCG AGC AAC		
	624		
20	Ser Lys Ala Lys Leu Val Pro Ser Glu Arg Glu Ala Ser Pro Ser Asn	195	200 205
	AGC TGC CAA GAC TCC ACG GAC ACC GAG AGC AAC AAC GAG GAG CAG CGC		
	672		
25	Ser Cys Gln Asp Ser Thr Asp Thr Glu Ser Asn Asn Glu Glu Gln Arg	210	215 220
	AGC GGT CTT ATC TAC CTG ACC AAC CAC ATC GCC CGA CGC GCG CAA CGC		
	720		
30	Ser Gly Leu Ile Tyr Leu Thr Asn His Ile Ala Arg Arg Ala Gln Arg	225	230 235 240
	GTG TCG CTC AAG GAG GAG CAC CGC GCC TAC GAC CTG CTG CGC GCC GCC		
	768		
35	Val Ser Leu Lys Glu Glu His Arg Ala Tyr Asp Leu Leu Arg Ala Ala	245	250 255
	TCC GAG AAC TCG CAG GAC GCG CTC CGC GTG GTC AGC ACC AGC GGG GAG		
	816		
40	Ser Glu Asn Ser Gln Asp Ala Leu Arg Val Val Ser Thr Ser Gly Glu	260	265 270
	CAG ATG AAG GTG TAC AAG TGC GAA CAC TGC CGG GTG CTC TTC CTG GAT		
	864		
45	Gln Met Lys Val Tyr Lys Cys Glu His Cys Arg Val Leu Phe Leu Asp	275	280 285
	CAC GTC ATG TAC ACC ATC CAC ATG GGC TGC CAC GGC TTC CGT GAT CCT		
	912		
50	His Val Met Tyr Thr Ile His Met Gly Cys His Gly Phe Arg Asp Pro	290	295 300
	TTT GAG TGC AAC ATG TGC GGC TAC CAC AGC CAG GAC CGG TAC GAG TTC		
	960		
55	Phe Glu Cys Asn Met Cys Gly Tyr His Ser Gln Asp Arg Tyr Glu Phe	305	310 315 320

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TCG TCG CAC ATA ACG CGA GGG GAG CAC CGC TTC CAC ATG AGC TA
1004

Ser Ser His Ile Thr Arg Gly Glu His Arg Phe His Met Ser
325 330

5

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 470 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

15

(v) FRAGMENT TYPE: C-terminal

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Xaa Xaa Ala Ser Asn Val Lys Val Glu Thr Gln Ser Asp Glu Glu Asn
1 5 10 15

25

Gly Arg Ala Cys Glu Met Asn Gly Glu Glu Cys Ala Glu Asp Leu Arg
20 25 30

Met Leu Asp Ala Ser Gly Glu Lys Met Asn Gly Ser His Arg Asp Gln
35 40 45

30

Gly Ser Ser Ala Leu Ser Gly Val Gly Gly Ile Arg Leu Pro Asn Gly
50 55 60

35

Lys Leu Lys Cys Asp Ile Cys Gly Ile Xaa Cys Ile Gly Pro Asn Val
65 70 75 80

Leu Met Val His Lys Arg Ser His Thr Gly Glu Arg Pro Phe Gln Cys
85 90 95

40

Asn Gln Cys Gly Ala Ser Phe Thr Gln Lys Gly Asn Leu Leu Arg His
100 105 110

Ile Lys Leu His Ser Gly Glu Lys Pro Phe Lys Cys His Leu Cys Asn
115 120 125

45

Tyr Ala Cys Arg Arg Arg Asp Ala Leu Thr Gly His Leu Arg Thr His
130 135 140

50

Ser Val Gly Lys Pro His Lys Cys Gly Tyr Cys Gly Arg Ser Tyr Lys
145 150 155 160

Gln Arg Xaa Ser Leu Glu Glu His Lys Glu Arg Cys His Asn Tyr Leu
165 170 175

55

Glu Ser Met Gly Leu Pro Gly Xaa Xaa Xaa Pro Val Ile Lys Glu Glu
180 185 190

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	Thr	Xaa	His	Xaa	Glu	Met	Ala	Glu	Asp	Leu	Cys	Lys	Ile	Gly	Xaa	Glu	
			195					200					205				
5	Arg	Ser	Leu	Val	Leu	Asp	Arg	Leu	Ala	Ser	Asn	Val	Ala	Lys	Arg	Lys	
		210					215					220					
	Ser	Ser	Met	Pro	Gln	Lys	Phe	Leu	Gly	Asp	Lys	Xaa	Leu	Ser	Asp	Xaa	
	225					230					235					240	
10	Pro	Tyr	Asp	Ser	Ala	Xaa	Tyr	Glu	Lys	Glu	Xaa	Xaa	Met	Met	Xaa	Ser	
					245					250					255		
	His	Val	Met	Asp	Xaa	Ala	Ile	Asn	Asn	Ala	Ile	Asn	Tyr	Leu	Gly	Ala	
15				260					265					270			
	Glu	Ser	Leu	Arg	Pro	Leu	Val	Gln	Thr	Pro	Pro	Gly	Xaa	Ser	Glu	Val	
			275					280					285				
20	Val	Pro	Val	Ile	Ser	Pro	Met	Tyr	Gln	Leu	His	Xaa	Xaa	Xaa	Ser	Xaa	
		290					295					300					
	Gly	Xaa	Pro	Arg	Ser	Asn	His	Ser	Ala	Gln	Asp	Xaa	Ala	Val	Xaa	Xaa	
	305					310					315					320	
25	Leu	Leu	Leu	Leu	Ser	Lys	Ala	Lys	Xaa	Val	Xaa	Ser	Glu	Arg	Glu	Ala	
					325					330					335		
	Ser	Pro	Ser	Asn	Ser	Cys	Gln	Asp	Ser	Thr	Asp	Thr	Glu	Ser	Asn	Xaa	
30				340					345					350			
	Glu	Glu	Gln	Arg	Ser	Gly	Leu	Ile	Tyr	Leu	Thr	Asn	His	Ile	Xaa	Xaa	
			355					360					365				
35	Xaa	Ala	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Lys	Glu	Glu	Xaa	Arg	Ala	Tyr	Xaa	
		370					375					380					
	Xaa	Leu	Arg	Ala	Ala	Ser	Glu	Asn	Ser	Gln	Asp	Ala	Xaa	Arg	Val	Val	
	385					390					395					400	
40	Ser	Thr	Ser	Gly	Glu	Gln	Xaa	Lys	Val	Tyr	Lys	Cys	Glu	His	Cys	Arg	
				405						410					415		
	Val	Leu	Phe	Leu	Asp	His	Val	Met	Tyr	Thr	Ile	His	Met	Xaa	Xaa	Xaa	
45				420					425					430			
	Gly	Cys	His	Gly	Phe	Arg	Asp	Pro	Phe	Glu	Cys	Asn	Met	Cys	Gly	Tyr	
			435					440					445				
50	His	Ser	Gln	Asp	Arg	Tyr	Glu	Phe	Ser	Ser	His	Ile	Thr	Arg	Gly	Glu	
		450					455					460					
	His	Arg	Xaa	His	Xaa	Ser											
	465					470											

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